

## RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/09/972,912

TIME: 09:53:02

Input Set : N:\Crf3\RULE60\09972912.raw

Output Set: N:\CRF3\01142002\I972912.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: SOPPET, DANIEL R.

6 RUBEN, STEVEN M.

8 (ii) TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE

10 (iii) NUMBER OF SEQUENCES: 42

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN &amp; FOX P.L.L.C.

14 (B) STREET: 1100 NEW YORK AVENUE, SUITE 600

15 (C) CITY: WASHINGTON

16 (D) STATE: DC

17 (E) COUNTRY: US

18 (F) ZIP: 20005-3934

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--&gt; 27 (A) APPLICATION NUMBER: US/09/972,912

C--&gt; 28 (B) FILING DATE: 10-Oct-2001

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 09/049,022

33 (B) FILING DATE:

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: STEFFE, ERIC K.

37 (B) REGISTRATION NUMBER: 36,688

38 (C) REFERENCE/DOCKET NUMBER: 1488.0620001

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: (202) 371-2600

42 (B) TELEFAX: (202) 371-2540

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 2745 base pairs

49 (B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

51 (D) TOPOLOGY: linear

53 (ii) MOLECULE TYPE: DNA (genomic)

56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 233..1423

60 (ix) FEATURE:

61 (A) NAME/KEY: sig\_peptide

62 (B) LOCATION: 233..328

64 (ix) FEATURE:

65 (A) NAME/KEY: mat\_peptide

ENTERED

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66 (B) LOCATION: 329..1423

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

71	GCAGCGGCAC	GGCAGCAGCG	GCAACAAGTG	CCGACTAGC	AGAGCCAAGC	CGGAGCAGTC	60
73	CCTGCCGCCG	ACACGCCCGG	GCCGCCCGTC	CGGGCGCCG	CGCATGGAGC	GTGAGCTGCG	120
75	GCGGTCGCCG	GGGCTGAGCC	GCGCGGAGCG	CCGGGACGTG	GATGTGGCCG	CGATCTCCCG	180
77	CCCTTGCCCC	CGCCCCCGG	AGCTGGAGCT	GCTCCCGGAC	AAGATATGAG	AA ATG	235
78					Met		
79					-32		
81	AGT GTT GGA	CGT CGA AGA	ATA AAG TTG	TTG GGT ATC	CTG ATG ATG	GCA	283
82	Ser Val Gly	Arg Arg Arg	Ile Lys Leu	Leu Gly Ile	Leu Met Met	Ala	
W--> 83	-30	-25	-20				
85	AAT GTC TTC	ATT TAT TTT	ATT ATG GAA	GTC TCC AAA	AGC AGT AGC	CAA	331
86	Asn Val Phe	Ile Tyr Phe	Ile Met Glu	Val Ser Lys	Ser Ser Ser	Gln	
W--> 87	-15	-10	-5			1	
89	GAA AAA AAT	GGA AAA GGG	GAA GTA ATA	ATA CCC AAA	GAG AAG TTC	TGG	379
90	Glu Lys Asn	Gly Lys Gly	Glu Val Ile	Ile Pro Lys	Glu Lys Phe	Trp	
91		5	10		15		
93	AAG ATA TCT	ACC CCT CCC	GAG GCA TAC	TGG AAC CGA	GAG CAA GAG	AAG	427
94	Lys Ile Ser	Thr Pro Pro	Glu Ala Tyr	Trp Asn Arg	Glu Gln Glu	Lys	
95		20	25		30		
97	CTG AAC CGG	CAG TAC AAC	CCC ATC CTG	AGC ATG CTG	ACC AAC CAG	ACG	475
98	Leu Asn Arg	Gln Tyr Asn	Pro Ile Leu	Ser Met Leu	Thr Asn Gln	Thr	
99		35	40		45		
101	GGG GAG GCG	GGC AGG CTC	TCC AAT ATA	AGC CAT CTG	AAC TAC TGC	GAA	523
102	Gly Glu Ala	Gly Arg Leu	Ser Asn Ile	Ser His Leu	Asn Tyr Cys	Glu	
103	50	55	60		65		
105	CCT GAC CTG	AGG GTC ACG	TCG GTG GTT	ACG GGT TTT	AAC AAC TTG	CCG	571
106	Pro Asp Leu	Arg Val Thr	Ser Val Val	Thr Gly Phe	Asn Asn Leu	Pro	
107		70	75		80		
109	GAC AGA TTT	AAA GAC TTT	CTG CTG TAT	TTG AGA TGC	CGC AAT TAT	TCA	619
110	Asp Arg Phe	Lys Asp Phe	Leu Leu Tyr	Leu Arg Cys	Arg Asn Tyr	Ser	
111		85	90		95		
113	CTG CTT ATA	GAT CAG CCG	GAT AAG TGT	GCA AAG AAA	CCT TTC TTG	TTG	667
114	Leu Leu Ile	Asp Gln Pro	Asp Lys Cys	Ala Lys Lys	Pro Phe Leu	Leu	
115		100	105		110		
117	CTG GCG ATT	AAG TCC CTC	ACT CCA CAT	TTT GCC AGA	AGG CAA GCA	ATC	715
118	Leu Ala Ile	Lys Ser Leu	Thr Pro His	Phe Ala Arg	Arg Gln Ala	Ile	
119		115	120		125		
121	CGG GAA TCC	TGG GGC CAA	GAA AGC AAC	GCA GGG AAC	CAA ACG GTG	GTG	763
122	Arg Glu Ser	Trp Gly Gln	Glu Ser Asn	Ala Gly Asn	Gln Thr Val	Val	
123	130	135	140		145		
125	CGA GTC TTC	CTG CTG GGC	CAG ACA CCC	CCA GAG GAC	AAC CAC CCC	GAC	811
126	Arg Val Phe	Leu Leu Gly	Gln Thr Pro	Pro Glu Asp	Asn His Pro	Asp	
127		150	155		160		
129	CTT TCA GAT	ATG CTG AAA	TTT GAG AGT	GAG AAG CAC	CAA GAC ATT	CTT	859
130	Leu Ser Asp	Met Leu Lys	Phe Glu Ser	Glu Lys His	Gln Asp Ile	Leu	
131		165	170		175		
133	ATG TGG AAC	TAC AGA GAC	ACT TTC TTC	AAC TTG TCT	CTG AAG GAA	GTG	907
134	Met Trp Asn	Tyr Arg Asp	Thr Phe Phe	Asn Leu Ser	Leu Lys Glu	Val	

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135	180	185	190	
137	CTG TTT CTC AGG TGG GTA AGT ACT TCC TGC CCA GAC ACT GAG TTT GTT	955		
138	Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe Val			
139	195 200 205			
141	TTC AAG GGC GAT GAC GAT GTT TTT GTG AAC ACC CAT CAC ATC CTG AAT	1003		
142	Phe Lys Gly Asp Asp Val Phe Val Asn Thr His His Ile Leu Asn			
143	210 215 220 225			
145	TAC TTG AAT AGT TTA TCC AAG ACC AAA GCC AAA GAT CTC TTC ATA GGT	1051		
146	Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile Gly			
147	230 235 240			
149	GAT GTG ATC CAC AAT GCT GGA CCT CAT CGG GAT AAG AAG CTG AAG TAC	1099		
150	Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys Tyr			
151	245 250 255			
153	TAC ATC CCA GAA GTT GTT TAC TCT GGC CTC TAC CCA CCC TAT GCA GGG	1147		
154	Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala Gly			
155	260 265 270			
157	GGA GGG GGG TTC CTC TAC TCC GGC CAC CTG GCC CTG AGG CTG TAC CAT	1195		
158	Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr His			
159	275 280 285			
161	ATC ACT GAC CAG GTC CAT CTC TAC CCC ATT GAT GAC GTT TAT ACT GGA	1243		
162	Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr Gly			
163	290 295 300 305			
165	ATG TGC CTT CAG AAA CTC GGC CTC GTT CCA GAG AAA CAC AAA GGC TTC	1291		
166	Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly Phe			
167	310 315 320			
169	AGG ACA TTT GAT ATC GAG GAG AAA AAC AAA AAT AAC ATC TGC TCC TAT	1339		
170	Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser Tyr			
171	325 330 335			
173	GTA GAT CTG ATG TTA GTA CAT AGT AGA AAA CCT CAA GAG ATG ATT GAT	1387		
174	Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile Asp			
175	340 345 350			
177	ATT TGG TCT CAG TTG CAG AGT GCT CAT TTA AAA TGC TAAAAATAGAT	1433		
178	Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys			
179	355 360 365			
181	ACAAACTCAA TTTTGCATAG AAAGGTGTAT TTTGAATAGT TCCCATGTTG TGTTCTCACA	1493		
183	TTAGAGTAAT TTCTATATTA AACCATGAAA ATTGCCTTTA TGAGTGATAC CCATTTGAGG	1553		
185	GCCTCTAAAC CCTTCAATTT GGTACTCACG TGAAGAGGGA AAGCGGAAGA TGGTAATTTT	1613		
187	TTTTTATGGA TGATATGGCA GGATGATTGG TTCTGATCTT ACCGGCTAGT GGTCATTTTT	1673		
189	AAAAAAGTTG TACCCTCTTA TCTGAAATCC TGTTTCTGGA ATTTGGCCAT TTAAAGTGAT	1733		
191	TTTGTTTGCC CTCTTCTATA ATATTCCTAC TTCCCATAAT AATGACTGAT TTATTTGTAA	1793		
193	TTCAGGTATT TATAAACCTA TTGGCTACAA AGACTTTGTT AAACATTATC CAGTGGTTTT	1853		
195	CGTGAAATGG AATTATGTTT ATTTTTATGG GATTTGGGTA AATTTTAAAT TGTCTAGAAA	1913		
197	ACTGAAATTT CAGTTGTCAG TTGTGGAATT CAGTTTTTCA ATTTGTGAAA TTTCCTGCCA	1973		
199	CCCCAACAGT ATTTTTGTGT GTTAATTAAT TTGCAAAAT GAGAATCATG GTGTGACACT	2033		
201	CATCTAATTT ATCTTGTTGT GATGTTATGG TCATAATAAG GAGAAAGAGG GTTTAATTTT	2093		
203	TCTTGATTTT GGTTTCCTGG TGGTATCATA GTGTAATTTT AGTATTTGAA AATCAGTGTG	2153		
205	ATTCCTTAAT GGCCAACTGA AGATTGAATT GCCGCTAACA ACCATATCGT GTTAGTGAAT	2213		
207	TTTCAATATG GACCAGGAAG GCATATGTAT TTTGAACTTG AGTGAAAAGG TTGAAGTTAC	2273		
209	AGACTTTTGC ATAGATGGTT TGTCAATTTA AAATTCCAGA ATTTATTATT GCCATATTTT	2333		

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211 CACATGCTGC TTATACAAGA TTATTATTGA GTAGTAAGTGT TTCCCTGTCT ATGTAGAAGT 2393
213 GCCTGTGTTT TTATTTATTG TTCCAGATCA AAGACCAAAA CATTTTCTTA AATATCTCTT 2453
215 ATGTAATATT TTATTTGTAT ACAGTGTGTG TGATGAAATA TTAACTAGA GCATGATATT 2513
217 TTAAATGTTA AGGTGTAACA TATGTTAAAT AAAACTGTTA TTTTGAATT TTAAAATTG 2573
219 TTTTTTGGGG GTATGAACCTA CTAGAGTTTA AAATTCTGCC AAATATTAC TTATATGTAC 2633
221 TATTGTGTAA CATACTTTCT TGAAATATTT TTGTTTATAG AATTGAAGGT TCTTATCAGA 2693
223 TGGGATACTG GGGATTATAA ACAATGGAAA TAAAGCCACT GTATTTTAA AA 2745
226 (2) INFORMATION FOR SEQ ID NO: 2:
228 (i) SEQUENCE CHARACTERISTICS:
229 (A) LENGTH: 397 amino acids
230 (B) TYPE: amino acid
231 (D) TOPOLOGY: linear
233 (ii) MOLECULE TYPE: protein
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
237 Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met
238 -32 -30 -25 -20
240 Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser
241 -15 -10 -5
243 Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe
244 1 5 10 15
246 Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu
247 20 25 30
249 Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
250 35 40 45
252 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
253 50 55 60
255 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
256 65 70 75 80
258 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
259 85 90 95
261 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
262 100 105 110
264 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala
265 115 120 125
267 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
268 130 135 140
270 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
271 145 150 155 160
273 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
274 165 170 175
276 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
277 180 185 190
279 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
280 195 200 205
282 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
283 210 215 220
285 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
286 225 230 235 240
288 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
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289					245					250					255		
291	Tyr	Tyr	Ile	Pro	Glu	Val	Val	Tyr	Ser	Gly	Leu	Tyr	Pro	Pro	Tyr	Ala	
292					260					265					270		
294	Gly	Gly	Gly	Gly	Phe	Leu	Tyr	Ser	Gly	His	Leu	Ala	Leu	Arg	Leu	Tyr	
295					275					280					285		
297	His	Ile	Thr	Asp	Gln	Val	His	Leu	Tyr	Pro	Ile	Asp	Asp	Val	Tyr	Thr	
298					290					295					300		
300	Gly	Met	Cys	Leu	Gln	Lys	Leu	Gly	Leu	Val	Pro	Glu	Lys	His	Lys	Gly	
301	305									310					315		320
303	Phe	Arg	Thr	Phe	Asp	Ile	Glu	Glu	Lys	Asn	Lys	Asn	Asn	Ile	Cys	Ser	
304					325					330					335		
306	Tyr	Val	Asp	Leu	Met	Leu	Val	His	Ser	Arg	Lys	Pro	Gln	Glu	Met	Ile	
307					340					345					350		
309	Asp	Ile	Trp	Ser	Gln	Leu	Gln	Ser	Ala	His	Leu	Lys	Cys				
310					355					360					365		
312	(2)	INFORMATION FOR SEQ ID NO: 3:															
314	(i)	SEQUENCE CHARACTERISTICS:															
315		(A) LENGTH: 323 amino acids															
316		(B) TYPE: amino acid															
317		(C) STRANDEDNESS: Not Relevant															
318		(D) TOPOLOGY: linear															
320	(ii)	MOLECULE TYPE: protein															
325	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 3:															
327	Gln	Ser	Lys	His	Arg	Lys	Leu	Leu	Leu	Arg	Cys	Leu	Leu	Val	Leu	Pro	
328	1				5					10					15		
330	Leu	Ile	Leu	Leu	Val	Asp	Tyr	Cys	Gly	Leu	Leu	Thr	His	Leu	His	Glu	
331					20				25					30			
333	Leu	Asn	Phe	Glu	Arg	His	Phe	His	Tyr	Pro	Leu	Asn	Asp	Asp	Thr	Gly	
334			35					40					45				
336	Ser	Gly	Ser	Ala	Ser	Ser	Gly	Leu	Asp	Lys	Phe	Ala	Tyr	Leu	Arg	Val	
337		50					55					60					
339	Pro	Ser	Phe	Thr	Ala	Glu	Val	Pro	Val	Asp	Gln	Pro	Ala	Arg	Leu	Thr	
340		65				70					75					80	
342	Met	Leu	Ile	Lys	Ser	Ala	Val	Gly	Asn	Ser	Arg	Arg	Arg	Glu	Ala	Ile	
343					85					90					95		
345	Arg	Arg	Thr	Trp	Gly	Tyr	Glu	Gly	Arg	Phe	Ser	Asp	Val	His	Leu	Arg	
346				100					105					110			
348	Arg	Val	Phe	Leu	Leu	Gly	Thr	Ala	Glu	Asp	Ser	Glu	Lys	Asp	Val	Ala	
349			115					120					125				
351	Trp	Glu	Ser	Arg	Glu	His	Gly	Asp	Ile	Leu	Gln	Ala	Asp	Phe	Thr	Asp	
352		130					135					140					
354	Ala	Tyr	Phe	Asn	Asn	Thr	Leu	Lys	Thr	Met	Leu	Gly	Met	Arg	Trp	Ala	
355		145				150					155					160	
357	Ser	Glu	Gln	Phe	Asn	Arg	Ser	Glu	Phe	Tyr	Leu	Phe	Val	Asp	Asp	Asp	
358					165</												

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09972912.raw

Output Set: N:\CRF3\01142002\I972912.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1